

GenCore version 5.1.3  
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# OM nucleic - nucleic search, using sw model

Run on: March 29, 2003, 21:10:37 ; Search time 531.339 Seconds

(without alignments)  
9201.802 Million cell updates/sec

Title: US-09-988-971-1\_COPY\_517\_684

Perfect score: 168

Sequence: 1 gccacagccgctgcccctg95.....gccccacgctgccaagtc 168

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: gb\_ba:\*  
2: gb\_hrg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_stg:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_un:\*  
28: em\_vl:\*  
29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rdn:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vtc:\*  
38: em\_by:\*  
39: em\_hgo\_hum:\*  
40: em\_hgo\_mus:\*  
41: em\_hgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	168	100.0	737	9	AF290986
2	168	100.0	786	9	AF290985
3	168	100.0	786	9	AF290983
4	168	100.0	2415	9	AK025635
5	168	100.0	2567	6	AK025645
6	166.4	99.0	1183	6	AX443133
7	166.4	99.0	1183	6	AX443135
8	124.8	74.3	1321	10	AF434990
9	124.8	74.3	1348	10	AF287467
10	90.8	54.0	66741	9	HS460J8
11	90.8	54.0	145833	2	AC026539
12	83.8	49.9	145068	9	HS037781
13	64.8	38.6	114096	2	AC123560
14	64.8	38.6	168498	2	AC125701
15	43.6	26.0	1518	9	HUMLYNTK
16	43.6	26.0	2288	9	HUMLYN
17	40	23.8	2044	10	MUSLYN
18	40	23.8	2703	10	MUSLYNB
19	40	23.8	2766	10	MUSLYNA
20	40	23.8	2938	10	BC031547
21	39	23.2	1076	9	HS030473
22	39	23.2	1870	9	BC007042
23	39	23.2	2021	9	HS044403
24	39	23.2	2109	6	AX428893
25	39	23.2	2665	6	AX335017
26	39	23.2	2665	6	D89077
27	38.8	23.1	1538	10	RATLYNTYR
28	38.8	23.1	1601	10	RATLYNTYR
29	38.8	23.1	2041	10	RNAF000300
30	38.8	23.1	2302	10	RNAF000301
31	38.8	23.1	2824	10	RNAF000302
32	38.8	23.1	3458	10	RATLYNTYRX
33	38	22.6	3701	5	CHRTCKL
34	38	22.6	4073	5	GGTKL
35	35.6	21.2	3921	5	XHCYBS
36	35.2	21.0	38681	1	SCBD9
37	34.4	20.5	1527	9	SSC277921
38	34.4	20.5	2032	9	HS1CKB
39	34.4	20.5	2032	9	HUM1CKA
40	34.4	20.5	139703	2	AC111951
41	34.4	20.5	173249	2	AC123468
42	34.4	20.5	180424	2	AC090496
43	34.2	20.4	1619	9	AB049594
44	34	20.2	2210	9	BC007371
45	34	20.2	2235	9	HSBIRPTK

## ALIGNMENTS

RESULT 1  
AF290986  
LOCUS  
DEFINITION Homo sapiens Src-like adaptor protein-2 splice isoform mRNA,  
ACCESSION AF290986  
VERSION AF290986.1 GI:17351922  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 737)  
Loreto, M.P. and McGlade, C.J.  
Direct Submission

Pred. No. is the number of results predicted by chance to have a

JOURNAL Submitted (28-JUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada

## FEATURES

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.7e-33;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## LOCUS

AF326353 786 bp mRNA linear PRI 08-NOV-2001

## DEFINITION

Homo sapiens Src-like adaptor protein-2 mRNA, complete cds.

## ACCESSION

AF326353

## VERSION

AF326353.1 GI:16797891

## KEYWORDS

Homo sapiens.

## ORGANISM

Homo sapiens.

## REFERENCE

Holland, S.J., Mendenhall, M.K., Zhou, X., Spencer, C., Pardo, J., Fu, A.C., Sheng, N., Shen, M., Liao, C., Luo, Y., Payan, D.G., Mancabo, H.S.Y., and Wu, J. Functional Cloning of Src-Like Adaptor Protein-2 (SLAP-2), a Novel Inhibitor of Antigen Receptor Signaling J. Exp. Med. 194 (9), 1263-1276 (2001)

## AUTHORS

Holland, S.J., Mendenhall, M.K., Zhou, X., Spencer, C., Pardo, J., Fu, A.C., Sheng, N., Shen, M., Liao, C., Luo, Y., Payan, D.G., Mancabo, H.S.Y., and Wu, J.

## TITLE

Direct Submission

## JOURNAL

Submitted (05-DEC-2000) Rigel Pharmaceutical Inc., 240 East Grand Avenue, South San Francisco, CA 94080, USA

## FEATURES

source

## CDS

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="20"

/feature\_type="mRNA"

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## BASE COUNT

162 a 234 c 231 g 159 t

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1 GCCACAGCCGCTGGCCCTGGCAGTTTCCGCGAGGTGCGCGCGCAGAGTGTGCTGAGA 60

## LOCUS

AF326353 786 bp mRNA linear PRI 08-NOV-2001

## DEFINITION

Homo sapiens Src-like adaptor protein-2 mRNA, complete cds.

## ACCESSION

AF326353

## VERSION

AF326353.1 GI:16797891

## KEYWORDS

Homo sapiens.

## ORGANISM

Homo sapiens.

## REFERENCE

Holland, S.J., Mendenhall, M.K., Zhou, X., Spencer, C., Pardo, J., Fu, A.C., Sheng, N., Shen, M., Liao, C., Luo, Y., Payan, D.G., Mancabo, H.S.Y., and Wu, J. Functional Cloning of Src-Like Adaptor Protein-2 (SLAP-2), a Novel Inhibitor of Antigen Receptor Signaling J. Exp. Med. 194 (9), 1263-1276 (2001)

## AUTHORS

Holland, S.J., Mendenhall, M.K., Zhou, X., Spencer, C., Pardo, J., Fu, A.C., Sheng, N., Shen, M., Liao, C., Luo, Y., Payan, D.G., Mancabo, H.S.Y., and Wu, J.

## TITLE

Direct Submission

## JOURNAL

Submitted (05-DEC-2000) Rigel Pharmaceutical Inc., 240 East Grand Avenue, South San Francisco, CA 94080, USA

## FEATURES

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/organism="Homo sapiens"

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Qy 121 GTCCTAGGACAGAGATTAACATCCCGACGCTCCAGCTGGCCAAAGTC 168  
Db 223 GTCCTAGGACAGAGATTAACATCCCGACGCTCCAGCTGGCCAAAGTC 270

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AK025645 2415 bp mRNA linear PRI 29-SEP-2000  
LOCUS Homo sapiens cDNA: FLJ21992 file, clone HEP06554.  
AK025645  
DEFINITION AK025645.1 GI:10438227  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE Homo sapiens hepatoma cell\_line:HEPG2 cDNA to mRNA, clone\_11b:HEP  
clone:HEP06554.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
1 (sites)  
Kawabata, A., Hiki, T., Kobayashi, N., Inagaki, H., Ikema, Y.,  
Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,  
Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.  
TITLE  
JOURNAL  
AUTHORS  
NEO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 2415)  
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,  
Shibahara, T., Tanaka, T. and Nakamura, Y.  
Direct Submission  
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure Analysis, Human  
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,  
Japan (E-mail: cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
Fax:81-3-5449-5416)

COMMENT  
NEO human cDNA sequencing project supported by Ministry of  
International Trade and Industry of Japan; cDNA full insert  
sequencing: Research Association for Biotechnology; cDNA library  
construction, 5' - & 3' - end one pass sequencing: Department of  
Virology and Human Genome Center, Institute of Medical Science,  
University of Tokyo (partly supported by Science and Technology  
Agency).

FEATURES  
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Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 5, 2e-33;  
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Qy 1 GCCACAGCCGCTGCGCTGCGCAGATTTCCTGGCAGAGTGCCTGGCAGAGCTGCTGAGAA 60  
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Db 223 CTCGGGAGGACCATTCATCTCTCTGAGATGAGACCTGGACGCTGTCTGAA 282  
Qy 121 GTCCTAGGACAGAGATTAACATCCCGACGCTCCAGCTGGCCAAAGTC 168  
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RESULT 5  
AX452880 2567 bp DNA linear PAT 06-JUL-2002  
LOCUS AX452880  
DEFINITION Sequence 1 from Patent WO0242457.  
ACCESSION AX452880  
VERSION AX452880.1 GI:21712520  
KEYWORDS  
SOURCE human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1  
Kang, H., Yang, W. P., Wu, Y., Whitney, G. S., Perez-Villar, J. J. and  
Kanner, S. B.  
TITLE  
JOURNAL  
AUTHORS  
Cloning and expression of human slap-2: a novel sh2/sh3  
domain-containing human slap homologue having immune cell-specific  
expression  
Patent: WO 0242457-A 1 30-MAY-2002;  
Bristol-Myers Squibb Co. (US)  
Location/Qualifiers

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/db\_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 5, 2e-33;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CTCGGGAGGACCATTCATCTCTCTGAGATGAGACCTGGACGCTGTCTGAA 120  
Db 577 CTCGGGAGGACCATTCATCTCTCTGAGATGAGACCTGGACGCTGTCTGAA 636  
Qy 121 GTCCTAGGACAGAGATTAACATCCCGACGCTCCAGCTGGCCAAAGTC 168  
Db 637 GTCCTAGGACAGAGATTAACATCCCGACGCTCCAGCTGGCCAAAGTC 684

RESULT 6  
AX443133 1183 bp DNA linear PAT 02-JUL-2002  
LOCUS AX443133  
DEFINITION Sequence 74 from Patent WO0216599.  
ACCESSION AX443133  
VERSION AX443133.1 GI:21690555  
KEYWORDS  
SOURCE human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1  
Burge, C. E., Conley, P. B., Grose, W. M., Hart, M., Kikuda, R.,  
Shimke, R. A., Spytak, K. A., Szekeres, E. S., Tomlinson, J. E.,  
Topper, J. N. and Yang, R. B.  
TITLE  
JOURNAL  
Proteins and nucleic acids encoding same  
Patent: WO 0216599-A 74 28-FEB-2002;  
Curagen Corporation (US); COR THERAPEUTICS, INC. (US)

FEATURES  
source  
1. 1183  
Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      251 a      359 c      333 g      240 t
ORIGIN

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Query Match	99.0%	Score 166.4	DB 6	Length 1183
Best Local Similarity	99.4%	Pred. No. 1.4e-32		
Matches 167; Conservative	0	Mismatches 1	Indels 0	Gaps 0

Qy 1 GCACACAGCCGTGGGCGCTGGGAGATTCCCGGCAAGTGGCCCGGACAGCTGTGGCTGAA 60

Db 500 GCCACAGCCGTGGGCGCTGGGCAATTCCCGGCAAGTGGCCCGGACAGCTGTGGCTGAA 550

Qy 61 CTCGGGAGACCATTGACCATCGTCTCTAGAGATGAGAGACGTGGACGCGTGTCTGAA 120

Db 560 CTCGGGAGACCATTGACCATCGTCTCTAGAGATGAGAGACGTGGACGCGTGTCTGAA 610

Qy 121 GTCCTAGGACGAGACTTAACATCAATCCCAAGCGTCAAGTGGCCAAAGTC 168

Db 620 GTCCTAGGACGAGACTTAACATCCCAAGCGTCAAGTGGCCAAAGTC 667

RESULT 7	AX443135/c	1183 bp	DNA	linear	PAT 02-JUL-2002
LOCUS	AX443135				
DEFINITION	Sequence 76 from Patent WO0216599.				
ACCESSION	AX443135				
VERSION	AX443135.1				
KEYWORDS	GI:21690556				
SOURCE	human.				
ORGANISM	Homo sapiens				

1  
 Buigues, C.E., Conley, P.B., Grosse, W.M., Hart, M., Kekuda, R.,  
 Shinkens, R.A., Spytek, K.A., Szekeres, E.S., Tomlinson, J.E.,  
 Topper, J.N., and Yang, R.B.  
 Proteins and nucleic acids encoding same  
 Patent: WO 0215599-A 76 28-FEB-2002;  
 Curagen Corporation (US); COR THERAPEUTICS, INC. (US)  
 Location/Qualifiers  
 1..1183

BASE COUNT	240 a	333 c	359 g	251 t
ORIGIN				

Query Match	99.0%	Score 166.4;	DB 6;	Length 1183;
Best Local Similarity	99.4%;	Pred. No. 1.4e-32;		
Matches 167;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

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Qy	61	CTGGGGGAGCCATTGACCACTGCTCTGTGAGATGAGAACTGTGTGAGACGTCGTCTGTGAA	12
Db	624	CTGGGGGAGCCATTGACCACTGCTCTGTGAGATGAGAACTGTGTGAGACGTCGTCTGTGAA	56
Qy	121	GTTCTCAGCGAGAGATTAATCAATCCCAAGCCCTCAAGTGGCCAAATC	168
Db	564	GTTCTCAGCGAGAGATTAATCAATCCCAAGCCCTCAAGTGGCCAAATC	517

RESULT 8	AF434990	1321 bp	RNA	linear	ROD 20-MAY-2002
LOCUS	AF434990				
DEFINITION	Mus musculus Src-like adapter protein-2 mRNA, complete cds.				
ACCESSION	AF434990				
VERSION	AF434990.1	GI:19224130			
KEYWORDS					
SOURCE	Mus musculus.				
ORGANISM	Mus musculus				

REFERENCE  
AUTHORS  
1 (Phases I to 1321)  
Eukaryota; Metazoa; Chordata; Crinatala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
Pander, A., Ibarrola, N., Krachmarova, I., Fernandez, M. M.,  
Condeelis, S. N., Ohara, O., Sawadkornol, S., Loidich, H. P. and  
Condeelis, S. N.

TITLE	A novel Src homology 2 domain-containing molecule, Src-like adapter protein-2 (SLAP-2), which negatively regulates T cell receptor signaling
JOURNAL	J. Biol. Chem. 277 (21), 19131-19138 (2002)
ENTRY TYPE	20012007

JOURNAL	J. Biol. Chem.	277	(21)	19131-19138	(2002)
MEDLINE	22013997				
PUBMED	11891219				
2	(bases 1 to 1321)				
AUTHORS	Ibarrola, N., Mann, M. and Pandey, A.				
TITLE	Direct Submissions				
JOURNAL	Submitted (16-Oct-2001)				
FEATURES	Whitehead Institute for Biomedical Research, Nine Cambridge Center, Cambridge, MA 02142, USA				
source	Location/Qualifiers				
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BASE COUNT ORIGIN	298 a	381 c	363 g	279 f
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Query Match	74.3%	Score 124.8	DB 10	Length 1321
Best Local Similarity	83.9%	Pred. No. 6.3e-22		
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 Db 373 GTCAACAGCTGTGGCCCTGGGCAAGTTCCCGGCAAGGTGAACAGGCCCAACATCTCTGGA 432  
 Oy 61 CTGGGGAGCCATTTGACCAATCTCTCTGAGAGATCGAGACTGTGAGACGGTCTGTAA 120  
 Db 433 CTGGGGAGCCGTGACCAATCTCTGTAGAGATGAGAGATGGTGTGACAGTCCAGTCGAA 492  
 Oy 121 GTCTCAGCAGAGAGATTAACATCTCCCAAGGCTCCACGTGGCAAAATC 168  
 Db 493 GTCTCAGCAGAGAGATTCACATCTCCCAAGTGTGTATGTGGTAAATC 540

LOCUS	AF287467	1348 bp	mRNA	linear	ROD 03-JUN-2002
DEFINITION	Mus musculus Src-like adaptor protein-2 mRNA, complete cds.				
ACCESSION	AF287467				
VERSION	AF287467.1	GI:17351918			

REFERENCE	1 (bases 1 to 1348)
AUTHORS	Loreto,M.P., Berry,D.M. and McGlade,C.J.
TITLE	Functional cooperation between c-Cbl and Src-like adaptor protein 2 in the negative regulation of T-cell receptor signaling
JOURNAL	Mol. Cell. Biol. 22 (12), 4241-4255 (2002)
MEDLINE	22022020
PUBMED	12024036
REFERENCE	2 (bases 1 to 1348)
AUTHORS	Loreto,M.P. and McGlade,C.J.
TITLE	Direct Submission

JOURNAL Submitted (14-JUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada

## FEATURES

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Best Local Similarity 83.9%; Pred. No. 6.3e-22;  
Matches 141; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 GCCACAGCCGTGGCCCTGGAGAGTTCCCGGAGAGTGGCCGAGCTGCTGCTAGA 60  
Db 381 GTCACAGCTGTGGCCCTGGAGAGTTCCCGGAGAGTGGCCGAGCTGCTGCTAGA 440  
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Db 441 CTCGGGAGAGCCCTGACCATCATCTCTGAGAGTGAAGTGTGTCACATCGCTG 500  
Qy 121 GTCTCAGGAGAGAGTAAACATCCCAAGCTGCACAGTGGCCAAATGC 168  
Db 501 GTCTCAGGAGAGAGTAAACATCCCAAGCTGCATGTGTATGTGCTAAATGC 548

RESULT 10  
HS4608/c 66741 bp DNA linear PRI 23-JUL-2001  
LOCUS  
DEFINITION Human DNA sequence from clone R33-4608 on chromosome 20q11.21-11.23 Contains the 3' end of the gene for a novel protein similar to N-myc downstream regulated (NDRG1) the 5' end of a gene encoding a novel protein tyrosine kinase, ESTs, STS and GSSs, complete sequence.

ACCESSION AL031662  
VERSION AL031662.26 GI:9716901  
KEYWORDS HTG; NDRG1; SH2 domain.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 66741)  
Skuce C

TITLE Direct Submission  
JOURNAL Submitted (23-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requesters: clonerequest@sanger.ac.uk  
On Aug 7, 2000 this sequence version replaced gi:6425549.

COMMENT During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

## FEATURES

## source

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/C/elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>  
IMPORTANT: This sequence is not the entire insert of clone R33-4608 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.  
The true right end of clone R33-4608 is at 66741 in this sequence. The true left end of clone R33-469A13 is at 41767 in this sequence. The true right end of clone R33-469A13 is at 4100 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. R33-4608 is from the library R33-3 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pCYPAC2

## Location/Qualifiers

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2375..2402  
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7486..7925  
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14248..14297  
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# TITLE JOURNAL COMMENT

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Testa, S., Theodore, J., Tittel, A., Travers, M., Triggillo, J.,  
Vassiliev, H., Vied, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 27, 2000 this sequence version replaced gi:17283243.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

## Project Information

Center project name: L7115

Center clone name: 712\_N\_14

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 125577 bases at least Q40

Consensus quality: 135703 bases at least Q30

Consensus quality: 135933 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 142233; sum-of-contigs

Quality coverage: 2.6 in Q20 bases; agarose-fp

Quality coverage: 3.3 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 37 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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5962 6061: gap of 100 bp
6062 7719: contig of 1658 bp in length
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7820 9799: contig of 1980 bp in length
9800 9899: gap of 100 bp
9900 11434: contig of 1535 bp in length
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14383 14482: gap of 100 bp
14483 17148: contig of 2666 bp in length
17149 17248: gap of 100 bp
17249 19239: contig of 1991 bp in length
19240 19339: gap of 100 bp
19340 21102: contig of 1763 bp in length
21103 21202: gap of 100 bp
21203 23371: contig of 2169 bp in length
23372 23471: gap of 100 bp
23472 25782: contig of 2311 bp in length
25783 25882: gap of 100 bp
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28825 28924: gap of 100 bp
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## FEATURES

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/db\_xref="taxon:9606"

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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,  
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 Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martin, E.,  
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 Weinsteck, G., and Gibbs, R.

\*\*\*\*\*  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 114096)  
 Morley, K. C.

\*\*\*\*\*  
 Direct Submission  
 Submitted (31-MAY-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 114096)  
 Morley, K. C.

\*\*\*\*\*  
 Direct Submission  
 Submitted (23-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 19, 2002 this sequence version replaced gi:21281284.

\*\*\*\*\*  
 Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu

\*\*\*\*\*  
 Project Information  
 Center project name: GXON  
 Center clone name: CH230-61622

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 Summary Statistics  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 92427 bases at least Q40  
 Consensus quality: 95724 bases at least Q30  
 Consensus quality: 98040 bases at least Q20

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 NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 33 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

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 57084 57185: gap of unknown length  
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 69738 73286: contig of 3548 bp in length  
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 73387 81837: contig of 8450 bp in length  
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 Best Local Similarity 78.0%; Prid. No. 9.9e-07;  
 Matches 78; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
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RESULT 14  
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 LOCUS  
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 AC125701.3 GI:22004133  
 HTG: HTGS PHASE1.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
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 Rattus.  
 1 (bases 1 to 168498)  
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 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
 Weinstein, G. and Gibbs, R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 168498)  
 Worley, K.C.  
 Direct Submission  
 Submitted (29-JUN-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 168498)  
 Worley, K.C.  
 Direct Submission  
 Submitted (31-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 30, 2002 this sequence version replaced gi:22002395.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center Project name: GDR  
 Center Clone name: CH230-12L23  
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 Consensus quality: 134611 bases at least Q30  
 Consensus quality: 140704 bases at least Q20  
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 NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/seqbank\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/seqbank_data.html)).  
 NOTE: This is a "working draft" sequence. It currently  
 consists of 56 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
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Best Local Similarity 78.0%; Fred. No. 9.5e-07;

Matches 78; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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RESULT 15  
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DEFINITION Human Lyn B protein mRNA, complete cds.
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AUTHORS Rader,U.G., Raben,N., Miller,L. and Jalsensma,C.
TITLE The cDNAs encoding two forms of the lyn protein tyrosine kinase are expressed in rat mast cells and human myeloid cells
JOURNAL Gene 138 (1-2), 219-222 (1994)
MEDLINE 94171041
PUBMED 8125304
REFERENCE 2 (bases 1 to 1518)
AUTHORS Miller,L.R. and Jalsensma,C.L.
TITLE Human promyeloid cells express two forms of the lyn protein tyrosine kinase
JOURNAL Unpublished
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reported here"
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ORIGIN

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Query Match 26.0%; Score 43.6; DB 9; Length 1518;

Best Local Similarity 58.5%; Fred. No. 0.38;

Matches 76; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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Oy 99 CTGTGAGACCGTCTGTCTGAAGTCTTCAGAGAGAGATTAACATCCCGAGCTCCAGT 158
Db 255 ATGTGAGAAAGCAAGTCCCTTTAACAAAAAGAGAGCTTATCCCGAGACACTATGT 314
Oy 159 GCCCAAGTC 168
Db 315 GCCCAACTC 324

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